

CC In AA021097, The peptides are used for the preparation of anti-canine
 CC 1 IgE antibody. The canine IgE antibody can be used for the diagnosis
 CC of canine allergies.

XX Sequence 20 AA:

Query Match 76.0% Score 100; DB 10; Length 20;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CFWNHGKPKVYVYVATA 19

1 | | | | | | | | | | | | | | | | | | | |

Db 2 CFWNHGKPKVYVYVATA 20

RESULT 2

AA050893 standard; Peptide; 17 AA.

XX AA050893:

DT 24-FEB-2000 (first entry)

XX Antibody 15A.2 binding peptide 10 from pNDCrC phage display library.

XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;

XX epitope; prophylaxis; treatment; minocone.

XX Synbatic.

XX EP957111.A2.

XX 17-MAY-1999.

PF 09-APR-1999; 98P-0107035.

XX 09-APR-1999; 98P-0083211.

PF 09-MAR-1999; 98P-0281760.

XX (IDEX-) IDEX LAB INC.

PI Lawton R, Nemmer B, Francoeur G;

XX WP1: 2000-04083/04.

PT Binding proteins used for treatment or prophylaxis of canine allergy -

PS Disclosure: Fig 6; 30pp; English.

CC This invention describes a novel binding protein which specifically
 CC binds to native canine IgE or B-cell bound IgE, and which doesn't bind
 CC to IgE when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC has a lesser or prophylactic or treatment or canine allergy.

CC AA079599 represent peptide mimotopes used in the method of the
 CC invention.

XX Sequence 17 AA:

Query Match 65.4% Score 89; DB 21; Length 17;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CFWNHGKPKVYVYVATA 16

1 | | | | | | | | | | | | | | | |

Db 2 CFWNHGKPKVYVYVATA 17

RESULT 3

AA050894 standard; Peptide; 17 AA.

XX AA050894:

DT 24-FEB-2000 (first entry)

XX Antibody 15A.2 canine IgE binding epitope 1.

XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;

XX epitope; prophylaxis; treatment; minocone.

XX Synbatic.

XX EP957111.A2.

XX 17-MAY-1999.

PF 09-APR-1999; 98P-0107035.

XX 09-APR-1999; 98P-0083211.

PF 30-MAR-1999; 98P-0281760.

XX (IDEX-) IDEX LAB INC.

PI Lawton R, Nemmer B, Francoeur G;

XX WP1: 2000-04083/04.

PT Binding proteins used for treatment or prophylaxis of canine allergy -

PS Disclosure: Fig 7; 30pp; English.

CC This invention describes a novel binding protein which specifically
 CC binds to native canine IgE or B-cell bound IgE, and which doesn't bind
 CC to IgE when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC has a lesser or prophylactic or treatment or canine allergy.

CC AA079599 represent peptide mimotopes used in the method of the
 CC invention.

XX Sequence 17 AA:

Query Match 65.4% Score 89; DB 21; Length 17;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CFWNHGKPKVYVYVATA 16

1 | | | | | | | | | | | | | | | |

Db 2 CFWNHGKPKVYVYVATA 17

RESULT 4

AA079599 standard; Peptide; 25 AA.

XX AA079599:

DT 15-MAY-2000 (first entry)

XX Optimized IgE-C3 domain antigen peptide for dog IgE.

XX Immunoglobulin E; IgE; antigen heavy chain; antigenic epitope;

XX antibody; allergy; allergic disease; immunization; anti-allergy;

XX anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

OS Canis sp.

Genome version 4.5
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OM protein - protein search, using sv model

Run on: July 15, 2002, 12:47:04 : Search time 12.87 seconds
(without alignments)
47487 Million cell updates/sec

Title: US-09-938-700-4

Percent score: 136

Sequence: 1 CATTGTCRFLRQVSLAANGKMAP 25

Scoring table: BLOSUM62

Gapop 10.0, -Gapart 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 13663

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Listing: All 4 summaries

Database: 1: Issued: protein.MAP
2: /cgn2.6/protein/2/1aa/79A.COMB.pep.*
3: /cgn2.6/protein/2/1aa/79A.COMB.pep.*
4: /cgn2.6/protein/2/1aa/79A.COMB.pep.*
5: /cgn2.6/protein/2/1aa/79A.COMB.pep.*
6: /cgn2.6/protein/2/1aa/79A.COMB.pep.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match length	DB ID	Description
1	64	47.1	25	US-09-100-4149-95
2	64	47.1	25	US-09-303-323-95
3	60	44.2	24	US-08-312-538-19
4	36	26.5	18	US-08-455-079-18
5	36	26.5	12	US-08-017-205-92
6	36	26.5	22	US-08-455-079-18
7	35.6	26.5	2	US-07-888-925-12
8	35.5	26.1	22	US-08-455-079-18
9	35.5	26.1	22	US-08-455-079-18
10	35.5	26.1	22	US-08-455-079-18
11	35.5	26.1	22	US-08-455-079-18
12	35.5	26.1	22	US-08-455-079-18
13	35.5	26.1	22	US-08-455-079-18
14	35.5	26.1	22	US-08-455-079-18
15	35.5	26.1	22	US-08-455-079-18
16	35.5	26.1	22	US-08-455-079-18
17	35.5	26.1	22	US-08-455-079-18
18	35.5	26.1	22	US-08-455-079-18
19	35.5	26.1	22	US-08-455-079-18
20	35.5	26.1	22	US-08-455-079-18
21	35.5	26.1	22	US-08-455-079-18
22	35.5	26.1	22	US-08-455-079-18
23	35.5	26.1	22	US-08-455-079-18
24	35.5	26.1	22	US-08-455-079-18
25	35.5	26.1	22	US-08-455-079-18
26	35.5	26.1	22	US-08-455-079-18
27	35.5	26.1	22	US-08-455-079-18

28	31.5	23.2	15	US-09-231-737-82	Sequence 87, Appl
29	31.5	23.2	15	US-08-455-079-18	Sequence 97, Appl
30	31.5	23.2	15	US-08-455-079-18	Sequence 97, Appl
31	31.5	23.2	15	US-08-455-079-18	Sequence 97, Appl
32	31.5	23.2	15	US-08-455-079-18	Sequence 97, Appl
33	31.5	23.2	15	US-08-455-079-18	Sequence 97, Appl
34	31.5	23.2	15	US-08-455-079-18	Sequence 97, Appl
35	31.5	23.2	15	US-08-455-079-18	Sequence 97, Appl
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37	31.5	23.2	15	US-08-455-079-18	Sequence 97, Appl
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41	31.5	23.2	15	US-08-455-079-18	Sequence 97, Appl
42	31.5	23.2	15	US-08-455-079-18	Sequence 97, Appl
43	31.5	23.2	15	US-08-455-079-18	Sequence 97, Appl
44	31.5	23.2	15	US-08-455-079-18	Sequence 97, Appl
45	31.5	23.2	15	US-08-455-079-18	Sequence 97, Appl

ALIGNMENTS

1	US-09-100-4149-95	location US/09100418
2	Retain No. 6025468	
3	GENERAL INFORMATION: Chang YI	
4	TITLE OF INVENTION: NOVEL LIRI PEPTIDE	
5	TITLE OF INVENTION: INVENTIONS	
6	INVENTOR: CHANG YI	
7	ADDRESS: 340 Park Avenue	
8	STATE: New York	
9	COUNTRY: USA	
10	COMPUTER READABLE FORM: YES	
11	OPERATING SYSTEM: PC Windows	
12	SOFTWARE: Word 97	
13	COMPARISON NUMBER: US/09100418	
14	FILE NAME: 20-JUNE-1998	
15	CLASSIFICATION: 20-212	
16	REGISTERED NUMBER: 20-212	
17	TELEPHONE: 212-751-4800	
18	TELECOMMUNICATION INFORMATION: 212-751-4800	
19	SEQUENCE CHARACTERISTICS:	
20	LENGTH: 100 amino acids	
21	TOPOLOGY: linear	
22	MOLECULAR TYPE: peptide	
23	US-09-100-4149-95	
24	Query Match	47.1%
25	Best Local Similarity	64.7%
26	Matches	11: Conservative 3: Mismatches 0: gaps 0: mismatches
27	8 KRYTHIRPHALAKSTIK 24	

Mon Jul 15 13:22:21 2002

us-09-938-700-4.closed.ra

Page 2

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SOFTWARE: MATHLIN (Greench)
 APPLICATION NUMBER: US/08/232,530D
 FILING DATE: 21-Apr-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/278593
 PRIOR APPLICATION DATA: 1994
 APPLICATION NUMBER: 07/714768
 ATTORNEY NAME: T. A. AUG-1991
 NAME: Synodak, Craig G.
 REGISTRATION NUMBER: 39, 044
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1489
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 TYPE: Amino acid
 TOPOLOGY: Linear
 US-08-232-530P-19
 44 19: Score 60: DB 23: Length 22:
 Match Local Similarity: 69.14%
 Matches 9: Conservative 3: Mismatch 0: Gaps 0
 QY 1 CAYHREHEDKIV 13
 DB 10 CAYHREHRAIM 22
 44 19: 1
 US-08-232-530P-20
 Sequence 20: Application US/0823590D
 Patent No. 5965709
 Inventor: Greench, David
 APPLICANT: Prosea, Leonard G.
 APPLICANT: Jarley, Paula M.
 NUMBER OF SEQUENCES: 60 Mismatch
 CORRESPONDENCE ADDRESS:
 STREET: 14000 Greench, Inc.
 CITY: South San Francisco
 COUNTY: California
 ZIP: 94080
 COMPUTER REMOTE FORM:
 NAME: Synodak, Craig G.
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MATHLIN (Greench)
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: US/08/232,530D
 CLASSIFICATION: 530, 1994
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION NUMBER: 07/714768
 FILING DATE: 07-JAN-1994
 APPLICATION DATA:
 FILING DATE: 07-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Synodak, Craig G.
 REGISTRATION NUMBER: 39, 044
 REFERENCE/DOCKET NUMBER: P071873
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1489
 TELEFAX: 650/932-9881

INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: L-AMINO ACIDS
 TOPOLOGY: Linear
 OS-08-231-5390-70

Query Match 44.1% Score 60; DB 2; Length 24;
 Best Local Similarity 69.2%; Pred. No. 26;
 Matches 5; Conservative 1; Mismatches 0; Gaps 0;
 Oy 1 CENTRHEP13
 Db 12 CENTRHEP14 24

RESULT 5
 US-09-017-205-52
 Sequence 52, Application US/09017205
 GENERAL INFORMATION:
 APPLICANT: Meriden, Rowland S
 TITLE OF INVENTION: PROTEIN 10 IS A POTENT INHIBITOR OF
 NUMBER OF SEQUENCES: 86
 COMPLETION DATE: 02-FEB-1999
 ADDRESS: Nixon & Vandecave PC
 STREET: 8th Floor, 1100 No. 5965357th Glabe Road
 CITY: Arlington
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22201-4714
 COMPUTER: IBM PC compatible
 SOFTWARE: Release 4.05, DOS
 CURRENT APPLICATION DATA: 09/07/205
 PUBLICATION DATE: 02-FEB-1999
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 29,009
 REFERENCE/DOCKET NUMBER: 604-435
 TELEPHONE: (703)816-4000
 TELEFAX: (703)816-4100
 INVENTOR: TOSATO, GIOVANNI
 LENGTH: 18 amino acids
 TYPE: amino acid
 MOLECULE TYPE: Peptide from HSV-2 glycoprotein g
 FRAGMENT TYPE: Internal
 OS-09-017-205-52

Query Match 26.5% Score 36; DB 2; Length 18;
 Best Local Similarity 75.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 2; Indels 0;
 Oy 4 TEPHEP11
 Db 7 TEPHEP14

RESULT 6
 US-08-455-079-18
 Sequence 18, Application US/08455079
 GENERAL INFORMATION:
 APPLICANT: TOSATO, GIOVANNI, L.L.P.
 TITLE OF INVENTION: PROTEIN 10 IS A POTENT INHIBITOR OF
 NUMBER OF SEQUENCES: 21
 COMPLETION DATE: 02-FEB-1999
 ADDRESS: MORGAN & PINDEMAN, L.L.P.
 STREET: NEW YORK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154
 COMPUTER READABLE FORM:
 REGISTRATION NUMBER: 34,596
 SOFTWARE: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA: 5.1
 FILING DATE: 31-MAY-1995
 NAME: KATHREN M. BROWN
 REGISTRATION NUMBER: 34,596
 TELEPHONE: (212) 756-4800
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: LINEAR
 OS-08-455-079-18

APPLICANT: TOSATO, GIOVANNI, L.L.P.
 TITLE OF INVENTION: PROTEIN 10 IS A POTENT INHIBITOR OF
 NUMBER OF SEQUENCES: 21
 COMPLETION DATE: 02-FEB-1999
 ADDRESS: MORGAN & PINDEMAN, L.L.P.
 STREET: NEW YORK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154
 COMPUTER READABLE FORM:
 REGISTRATION NUMBER: 34,596
 SOFTWARE: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA: 5.1
 FILING DATE: 31-MAY-1995
 NAME: KATHREN M. BROWN
 REGISTRATION NUMBER: 34,596
 TELEPHONE: (212) 756-4800
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: LINEAR
 OS-08-455-079-18

Query Match 28.5% Score 36; DB 2; Length 22;
 Best Local Similarity 31.2%; Pred. No. 26;
 Matches 5; Conservative 6; Mismatches 3; Indels 0;
 Oy 10 ADVESIMANORAP 25
 Db 7 KILIANORAP 22

RESULT 7
 US-08-455-079-14
 Sequence 14, Application US/08455079
 GENERAL INFORMATION:
 APPLICANT: TOSATO, GIOVANNI, L.L.P.
 TITLE OF INVENTION: PROTEIN 10 IS A POTENT INHIBITOR OF
 NUMBER OF SEQUENCES: 21
 COMPLETION DATE: 02-FEB-1999
 ADDRESS: MORGAN & PINDEMAN, L.L.P.
 STREET: NEW YORK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154
 COMPUTER READABLE FORM:
 REGISTRATION NUMBER: 34,596
 SOFTWARE: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA: 5.1
 FILING DATE: 31-MAY-1995

us-09-938-700-4.closed.ra1

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1  ATTORNEY/AGENT INFORMATION:
2  NAME: KATHRYN M. BROWN
3  REGISTRATION NUMBER: 34,566
4  REFERENCE/DOCKET NUMBER: 2076-4187
5  TITLE/COMPLAINT INFORMATION:
6  TELEPHONE: (212) 758-4800
7  TELEFAX: (212) 751-6649
8  FAX: (212) 751-6649
9  INFORMATION FOR SEQ ID NO: 1:
10  SEQUENCE CHARACTERISTICS:
11  LENGTH: 23 AMINO ACIDS
12  TYPE: AMINO ACID
13  TOPOLOGY: LINEAR
14  MOLECULE TYPE: PEPTIDE
15  OS-MOL-4-55-079-14

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US-07-988-925-12

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COMPILED READING FORM:
 COMPUTER: IBM PC
 OPERATING SYSTEM: PC-DOS
 CURRENT APPLICATION RELEASE: 1.0
 APPLICATION NUMBER: 08/07/988,925
 CLIPPING DATE:
 CLIPPING FROM: 424
 PAPER APPLICATION DATE:
 APPLICATION NUMBER: DB 9504422,9
 PAPER DATE: 1992-04-16
 PAPER APPLICATION NUMBER: 00 PBT/90/1393
 ATTENDING DATE: 21-02-1992
 NAME: HITCHCOCK DOOR C
 REGISTRATION NUMBER: 2009
 TELEPHONE NUMBER: 0000000000
 TELEFAX: 70881454100
 INFORMATION FOR SEND TO NO: 12:
 SOURCE: SEARCHED
 LENGTH: 22 amino acids
 TYPE: amino acid
 TOWARDNESS: single
 MOLECULE TYPE: peptide

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Query Match      26.1% Score 35.5 Db 1 Length 22:
Beet local similarity 35.0%
Matches 7: Conservative 5: Mismatches 1: Indels 7: Gaps 1:

3 VTRHPRLPROVSIANARGK 22
|||
4 LTQPH-----SYSESPGK 16

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RESULT: 9
 US-08-362-780-12
 Sequence 12, Application US/08362780
 Patent No. 5968509
 GENERAL INFORMATION:
 APPLICANT: Gorman, Scott D
 APPLICANT: Roulledge, Edward G
 APPLICANT:

1 TITLE OF INVENTION: Antibody Preparation
2
3 NUMBER OF SEQUENCES: 26
4
5 CORRESPONDENCE ADDRESS:
6
7 ADDRESSEE: Nixon and Vanderhye PC
8 STREET: 8th Floor, 1100 NO. 5968509th Glebe Road
9 CITY: Arlington
10 STATE: Virginia
11 COUNTRY: USA
12
13 ZIP: 22201

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PRTIN APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/GB91/01726
 FILING DATE: 10-06-91
 ATTORNEY/AGENCY: 10-06-91
 NAME: Mitchell, David C
 REGISTRATION NUMBER: 29009
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 7030161400
 TELEFAX: 7030161400
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 STRATEGY: single
 TOPOLOGY: linear
 MOLECULE TYPE: polypeptide
 S-08-562-780-12

Query Match	26.11	Score 36.5	DB 2	Length 22
Beet Local Similarity	35.04			Pred. No. 31
Matches	7	Conservative	5	Mismatches
				1. Indels
				7. Gaps
3 VTHPHLPDYNSIAKAPCK	22			
4 LTPH-----SVSSPCK	16			

RESULT 10
US-09-046-985-4

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Sequence 4: Application US/09/046/985
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PLOTTER IN Release #1.0, Version #1.30
COMPILER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPILED: IBM PC COMPATIBLE
CURRENT APPLICATION DATA: user #1.0, Version #1.30
APPLICATION NUMBER: US/09/046/985
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, David E. 21 592
OTHER INFORMATION: /label=modified site
REFERENCE/DOCID NUMBER: CMC-614
TELEPHONE: (781) 861-9540
TELEFAX: (781) 861-9540
INFORMATION FOR SLD ID NO. 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
STRANDNESS: 4218
TOPOLGY: linear
FEATURE: type: peptide
MOLECULE TYPE: peptide
PATTERN: modified-site
LOCATION: 1
OTHER INFORMATION: /label=modified an
US-09-938-700-4
Query Match 25 %; Score 35; DB 3; Length 22;
Real Local Similarity 40.0% Pval NO. 37
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
DB 8 HRPDUSVYRABG 22

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Sequence 4: Application US/09/046/985
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PLOTTER IN Release #1.0, Version #1.30
COMPILER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPILED: IBM PC COMPATIBLE
CURRENT APPLICATION DATA: user #1.0, Version #1.30
APPLICATION NUMBER: US/09/046/985
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, David E. 22 592
OTHER INFORMATION: /label=modified site
REFERENCE/DOCID NUMBER: CMC-614
TELEPHONE: (781) 861-9540
TELEFAX: (781) 861-9540
INFORMATION FOR SLD ID NO. 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
STRANDNESS: 4218
TOPOLGY: linear
FEATURE: type: peptide
MOLECULE TYPE: peptide
PATTERN: modified-site
LOCATION: 1
OTHER INFORMATION: /label=modified an
US-09-938-700-4
Query Match 25 %; Score 35; DB 4; Length 22;
Real Local Similarity 40.0% Pval NO. 37
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
DB 8 HRPDUSVYRABG 22

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Sequence 4: Application US/09/046/985
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PLOTTER IN Release #1.0, Version #1.30
COMPILER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPILED: IBM PC COMPATIBLE
CURRENT APPLICATION DATA: user #1.0, Version #1.30
APPLICATION NUMBER: US/09/046/985
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, David E. 21 592
OTHER INFORMATION: /label=modified site
REFERENCE/DOCID NUMBER: CMC-614
TELEPHONE: (781) 861-9540
TELEFAX: (781) 861-9540
INFORMATION FOR SLD ID NO. 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
STRANDNESS: 4218
TOPOLGY: linear
FEATURE: type: peptide
MOLECULE TYPE: peptide
PATTERN: modified-site
LOCATION: 1
OTHER INFORMATION: /label=modified an
US-09-938-700-4
Query Match 25 %; Score 35; DB 3; Length 22;
Real Local Similarity 40.0% Pval NO. 37
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
DB 8 HRPDUSVYRABG 22

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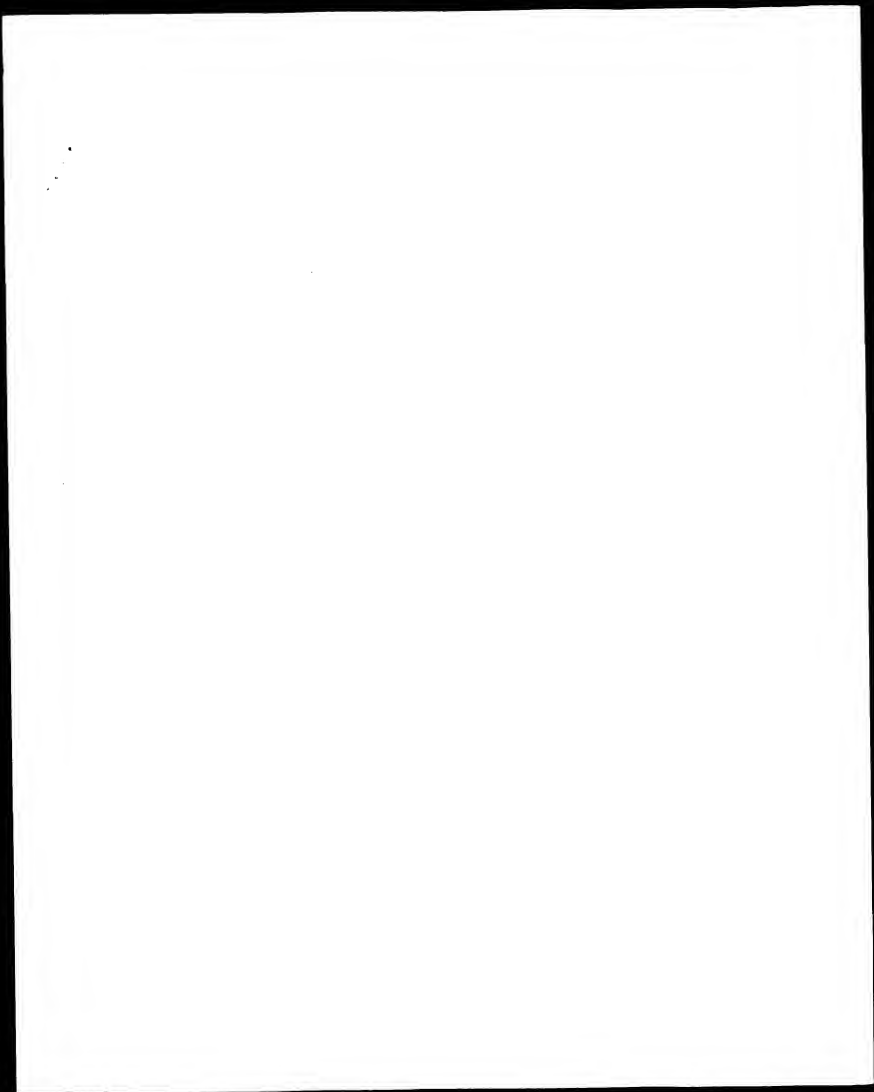
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PLOTTER IN Release #1.0, Version #1.30
COMPILER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPILED: IBM PC COMPATIBLE
CURRENT APPLICATION DATA: user #1.0, Version #1.30
APPLICATION NUMBER: US/09/046/985
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, David E. 22 592
OTHER INFORMATION: /label=modified site
REFERENCE/DOCID NUMBER: CMC-614
TELEPHONE: (781) 861-9540
TELEFAX: (781) 861-9540
INFORMATION FOR SLD ID NO. 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
STRANDNESS: 4218
TOPOLGY: linear
FEATURE: type: peptide
MOLECULE TYPE: peptide
PATTERN: modified-site
LOCATION: 1
OTHER INFORMATION: /label=modified an
US-09-938-700-4
Query Match 25 %; Score 35; DB 4; Length 22;
Real Local Similarity 40.0% Pval NO. 37
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
DB 8 HRPDUSVYRABG 22

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SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/430,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION NUMBER: US 08/951,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/946,017
 FILING DATE: 05-MAY-1997
 CLASSIFICATION: 516-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/944,419
 FILING DATE: 05-MAY-1997
 CLASSIFICATION: 516
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 CLASSIFICATION: 516-1996
 NAME: Apple, Randolph F.
 REGISTRATION NUMBER: 36,429
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 INFORMATION FOR SEQ ID NO: 208:
 SEQUENCE CHARACTERISTICS: 408:
 LENGTH: 23 amino acids
 STANDARD: amino acid
 TOPOLOGY: linear
 US-08-951,050-208
 Query Match
 Best Local Similarity: 25.7%, Score 35, DB 4, Length 23;
 Matches 10, Conservative 1, Mismatches 3, Indels 12, Gaps 2;
 Oy 4 TRH-----LFDVSIIMAKRGAP 25
 Db 6 TSHRNRMKD-----FGRKCP 23

SEQUENCE: 15
 US-09-430-323-208
 Sequence 208, Application US/09430323
 Patent No. 6309657
 TITLE OF INVENTION:
 APPLICATION: Cecchi, Thomas R.
 Attorney: Joachim
 Moriio, Gregg B.
 Chapman, Aaron B.
 Address: 2000 California
 STATE: California
 COUNTRY: United States of America
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: compatible
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/430,323
 FILING DATE: 29-OCT-1999
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION NUMBER: US 08/954,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/951,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/946,017
 FILING DATE: 05-MAY-1997
 APPLICATION NUMBER: US 08/944,419
 FILING DATE: 18-APR-1997
 FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph F.
 REGISTRATION NUMBER: 36,429
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 INFORMATION FOR SEQ ID NO: 208:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-09-430-323-208
 Query Match
 Best Local Similarity: 25.7%, Score 35, DB 4, Length 23;
 Matches 10, Conservative 1, Mismatches 3, Indels 12, Gaps 2;
 Oy 4 TRH-----LFDVSIIMAKRGAP 25
 Db 6 TSHRNRMKD-----FGRKCP 23

Search completed: July 15, 2002, 12:50:38
 Job time: 214 sec



Query Match 19.1k: Score 26; DB 2; Length 24;
 Best Local Similarity 40.0k; Pred. No. 3.3e+03;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Oy 15 SIMAMPERKA 24
 Db 10 TUSPREFRAN 19
 :::::|||||

SEQUENCE 14
 JP0052
 C:Species: Macula maculata (fragment)
 C:Accession: JP0052
 C:Release: Nov-1994
 C:Accession: JP0052
 R:Ogil, K. to JIPID, February 1994
 A:Description: phylogenetic diversity in the genus bacillus and comparative ribosomal po
 A:Reference number: JP0042
 A:Accession: JP0052
 A:Molecule type: protein
 A:Residues: 1-24 GCGCG
 C:Superfamily: 1.24 GCGCG
 C:Keywords: protein bioglycals; ribosome

Query Match 19.1k: Score 26; DB 2; Length 24;
 Best Local Similarity 50.0k; Pred. No. 3.3e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 12 TNSIMAMFC 21
 Db 8 LYNSTLARG 17
 ::|||::||

RESULT 15
 N:1538
 N:1538
 N:1538
 C:Species: bradykinin-potentiating peptide 8 - island jareca
 C:Accession: A37196
 C:Release: Dec-1992
 C:Accession: A37196
 R:Gentry, A.C.O.; Vieira, C.A.; Gagliolo, J.R.
 A:Description: bradykinin-potentiating peptide 8 - island jareca
 A:Reference number: A37196; MIMD:9051557
 A:Accession: A37196
 A:Molecule type: protein
 A:Residues: 1-10 GCGCG
 C:Superfamily: 1.10 GCGCG
 C:Keywords: pyroglutamate; pyroglutamic acid
 F:1/Modified sites: pyroglutamate carboxylic acid (Gln) status experimental

Query Match 18.4k: Score 25; DB 2; Length 10;
 Best Local Similarity 60.0k; Pred. No. 1.3e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 5 HPLP 9
 Db 5 HPLP 9

Search completed: July 15, 2002, 12:50:59
 Job time: 120 sec

Genome version 4.5
Copyright (c) 1993 - 2000 Comagen Ltd.

On protein - protein search, using sw model

Run on: July 15, 2002, 13:50:44 : Search time 10.22 seconds

(Without alignments)
34/715 million cell updates/sec

Title: US-09-938-700-4

Perfect score: 1.6
Sequence: 1 CMTVPRHPLADIVRISAMANGRRAP 25

Scoring table: BLOSUM62
Gap: 10.0, Gapext: 0.5

Searched: 105234 seqs, 38719350 residues

Total number of hits satisfying chosen parameters: 1503

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum match 0%

Maximum match 100%

Database: SwissProt_40*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the reported score. The score is printed, and is derived by analysis of the score score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB ID	Description
1	31	22.8	18	1	CTCA_LITCI	P81844 Iltoria ctt
2	29	21.3	18	1	CTCA_LITCI	P81838 Iltoria ctt
3	29	19.3	17	1	PR4_PRRM	P82619 periplasma
4	27	19.9	24	1	DN66_PRR1	P81490 phyllotheus
5	27	19.9	24	1	YOL_0R03	P81452 bacteriophus
6	26	19.9	13	1	PR71_LITRM	P82050 Iltoria eal
7	26	19.1	13	1	OC05_XM4E	P80612 zea mays (e
8	26	19.1	13	1	OC05_XM4E	P81485 Iltoria ctt
9	26	19.1	13	1	OC05_XM4E	P81485 Iltoria ctt
10	26	19.1	13	1	OC05_XM4E	P81485 Iltoria ctt
11	26	19.1	13	1	OC05_XM4E	P81485 Iltoria ctt
12	26	18.4	10	1	BRP8_BOTIN	P81426 bathyops in
13	25	18.4	10	1	BRP8_BOTIN	P81426 bathyops in
14	25	18.4	10	1	BRP8_BOTIN	P81426 bathyops in
15	25	18.4	10	1	BRP8_BOTIN	P81426 bathyops in
16	25	18.4	10	1	BRP8_BOTIN	P81426 bathyops in
17	25	18.4	10	1	BRP8_BOTIN	P81426 bathyops in
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Result	No.	Score	Match	Length	DB ID	Description
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2	35	23	16.9	10	1	ANZ_LITRA
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4	37	23	16.9	10	1	R811_RAND
5	38	23	16.9	10	1	LIC_SINIC
6	38	23	16.9	10	1	LIC_SINIC
7	40	23	16.9	20	1	SDM_LORR
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9	41	23	16.9	21	1	CPY_PRRH
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ALIGNMENTS

Result	No.	Score	Match	Length	DB ID	Description
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2	35	23	16.9	10	1	ANZ_LITRA
3	35	23	16.9	10	1	ANZ_LITRA
4	37	23	16.9	10	1	R811_RAND
5	38	23	16.9	10	1	LIC_SINIC
6	38	23	16.9	10	1	LIC_SINIC
7	40	23	16.9	20	1	SDM_LORR
8	40	23	16.9	20	1	SDM_LORR
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22	42	23	16.9	21	1	CPY_PRRH
23	42	23	16.9	21	1	CPY_PRRH
24	42	23	16.9	21	1	CPY_PRRH
25	42	23	16.9	21	1	CPY_PRRH
26	42	23	16.9	21	1	CPY_PRRH
27	42	23	16.9	21	1	CPY_PRRH
28	42	23	16.9	21	1	CPY_PRRH
29	42	23	16.9	21	1	CPY_PRRH
30	42	23	16.9	21	1	CPY_PRRH
31	42	23	16.9	21	1	CPY_PRRH
32	42	23	16.9	21	1	CPY_PRRH
33	42	23	16.9	21	1	CPY_PRRH
34	42	23	16.9	21	1	CPY_PRRH
35	42	23	16.9	21	1	CPY_PRRH
36	42	23	16.9	21	1	CPY_PRRH
37	42	23	16.9	21	1	CPY_PRRH
38	42	23	16.9	21	1	CPY_PRRH
39	42	23	16.9	21	1	CPY_PRRH
40	42	23	16.9	21	1	CPY_PRRH
41	42	23	16.9	21	1	CPY_PRRH
42	42	23	16.9	21	1	CPY_PRRH
43	42	23	16.9	21	1	CPY_PRRH
44	42	23	16.9	21	1	CPY_PRRH
45	42	23	16.9	21	1	CPY_PRRH

the 1990s, the number of people in the world who are under 15 years of age has increased from 1.1 billion to 1.5 billion, and the number of people aged 65 and over has increased from 0.2 billion to 0.5 billion (United Nations 1999). The United Nations predicts that by the year 2050, the number of people aged 65 and over will be 1.1 billion, and the number of people under 15 years of age will be 1.1 billion (United Nations 1999).

There are a number of reasons why the number of people aged 65 and over is increasing. One reason is that people are living longer. The life expectancy at birth in the United Kingdom has increased from 72 years in 1950 to 77 years in 1995 (Office for National Statistics 1996). Another reason is that the number of people aged 65 and over is increasing because of the increase in the number of people aged 65 and over who are surviving. The number of people aged 65 and over who are surviving has increased from 0.1 billion in 1950 to 0.4 billion in 1995 (Office for National Statistics 1996).

The increase in the number of people aged 65 and over is a major challenge for the United Kingdom. The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing. The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing. The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing.

The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing. The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing. The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing.

The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing. The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing. The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing.

The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing. The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing. The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing.

The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing. The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing. The United Kingdom has a large number of people aged 65 and over, and the number of people aged 65 and over is increasing.

Best Local Similarity: 46.7%; Pred. No. 3.2e+03;
Matches 17; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 6 PHILIPININAMP 20
Db 2 PLEKOPHMANMP 16

RESULT 11

Qy 0979M3 PRELIMINARY; PRT: 17 MA.

AC 0979M3
DT 01-MAY-2000 (TRENBERGEL, 13, Created)
DT 01-MAY-2000 (TRENBERGEL, 13, Last sequence update)
DE TYPE IV PROCOPIININAMP (FRAGMENT)
OS Trypanosoma cruzi.
OC Trypanosoma cruzi.
OK NCBI_Taxid=5593
RN SOURCE

RA MEDLINE=9401310 PubMed=9221715;
RA Toro G.C., Galanti N., Helman D., Wernstedt C.;
RT Identification and localization of histone H1 in Trypanosoma cruzi.
RJ J Biol Chem 271:1807-1811(1996).
SL SOURCE 17 MA: 1807 MW: A019CC3208RCD5 CR664;

Query Match 19.5%; Score 26.5; DB 5; Length 17;
Best Local Similarity: 40.0%; Pred. No. 3.1e+03;
Matches 0; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

Qy 9 PRODIYANAMP 23
Db 6 PLEKOPHMANMP 17

RESULT 12

Qy 0979M3 PRELIMINARY; PRT: 22 MA.

AC 0979M3
DT 01-MAY-2000 (TRENBERGEL, 13, Created)
DT 01-MAY-2000 (TRENBERGEL, 13, Last sequence update)
DE POLYDIACTINONE INDOLOPHANINAMP (FRAGMENT)
OS Onchocerca oregonensis (Swamp pinworm).
OC Onchocerca oregonensis (Swamp pinworm).
OK NCBI_Taxid=94345
RN SOURCE

RA MEDLINE=93005658 PubMed=1232116;
RA Characterization of a novel family abundantly expressed in Onchocerca
RT oregonensis pollen that shows sequence similarity to
RJ Plant Cell 22:2837-2847(1990).
SL SOURCE 22 MA: 2837 MW: 238F8F8A1F8C70 CR664;

Query Match 19.5%; Score 26.5; DB 10; Length 22;
Best Local Similarity: 38.1%; Pred. No. 4e+03;
Matches 9; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

Qy 1 CENTRIPOLYDINAMP 21
Db 1 CTTINQ-POLYDINAMP 20

RESULT 13

Qy 099C8 PRELIMINARY; PRT: 15 MA.

AC 099C8

AC 099C8

DT 01-MAY-2000 (TRENBERGEL, 13, Created)
DT 01-MAY-2000 (TRENBERGEL, 13, Last sequence update)
DE TYPE IV PROCOPIININAMP (FRAGMENT)
OS Homo sapiens (human).
OC Homo sapiens (human).
OK NCBI_Taxid=5606
RN SOURCE

RA MEDLINE=93135366 PubMed=1480041;
RA Steinhilber M.G., Krizschak H.C., Lottia L.A.;
RT Metalloproteinases (MMPs) and characterization of a new member of the
RJ Matrix Suppl. 1:359-366(1992).
SL SOURCE 15 MA: 1537 MW: D04AAAP32276C CR664;

Query Match 19.1%; Score 26; DB 4; Length 15;
Best Local Similarity: 60.0%; Pred. No. 3.0e+03;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 16 IAKKOPV 25
Db 5 IAKKOPV 14

RESULT 14

Qy 0979M3 PRELIMINARY; PRT: 16 MA.

AC 0979M3
DT 01-MAY-2000 (TRENBERGEL, 13, Created)
DT 01-MAY-2000 (TRENBERGEL, 13, Last sequence update)
DE 2-INOTY-COA HYDRATASE (FRAGMENT).
OS Homo sapiens (human).
OC Homo sapiens (human).
OK NCBI_Taxid=5606
RN SOURCE

RA MEDLINE=9504784 PubMed=7958199;
RA Middleton B.;
RT The mitochondrial long-chain trifunctional enzyme, 2-enoyl-CoA
RJ Hydratase, is involved in the degradation of long-chain fatty acids.
RJ Biochem Soc Trans 22:427-431(1994).
SL SOURCE 16 MA: 427 MW: 31A06A3080079A CR664;

Query Match 19.1%; Score 26; DB 8; Length 16;
Best Local Similarity: 31.2%; Pred. No. 3.0e+03;
Matches 5; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 10 KDNVSKAKK 25
Db 1 KDNVSKAKK 16

RESULT 15

Qy 095A2 PRELIMINARY; PRT: 18 MA.

AC 095A2
DT 01-DEC-2001 (TRENBERGEL, 13, Created)
DT 01-DEC-2001 (TRENBERGEL, 13, Last sequence update)
DE MYOININ ALPINA 2 SUBUNIT (FRAGMENT).
OS Homo sapiens (human).
OC Homo sapiens (human).
OK NCBI_Taxid=5606
RN SOURCE

Mon Jul 15 13:22:25 2002

us-09-938-700-4.closed.rpt

Page 5

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RN      [1]
RP
RC      SEQUENCE FROM N.A.
RC
RC      TISSUE-CARDIOVASCULAR:
RC      Mirmiran A., Kneese R.
RC      *Regulation of VSMC Differentiation.*
RC      Submitted (DEC-2000) to the ENCL/Genbank/CDDB databases
DR      ENBL, A13340200, AAL03465.1.
FT
FT      NON_TER      1
FT      NON_TER      1
FT      NON_TER      1
FT      SEQUENCE_18   18      DFEA4C6E1A5B0EF C6C64:
FO

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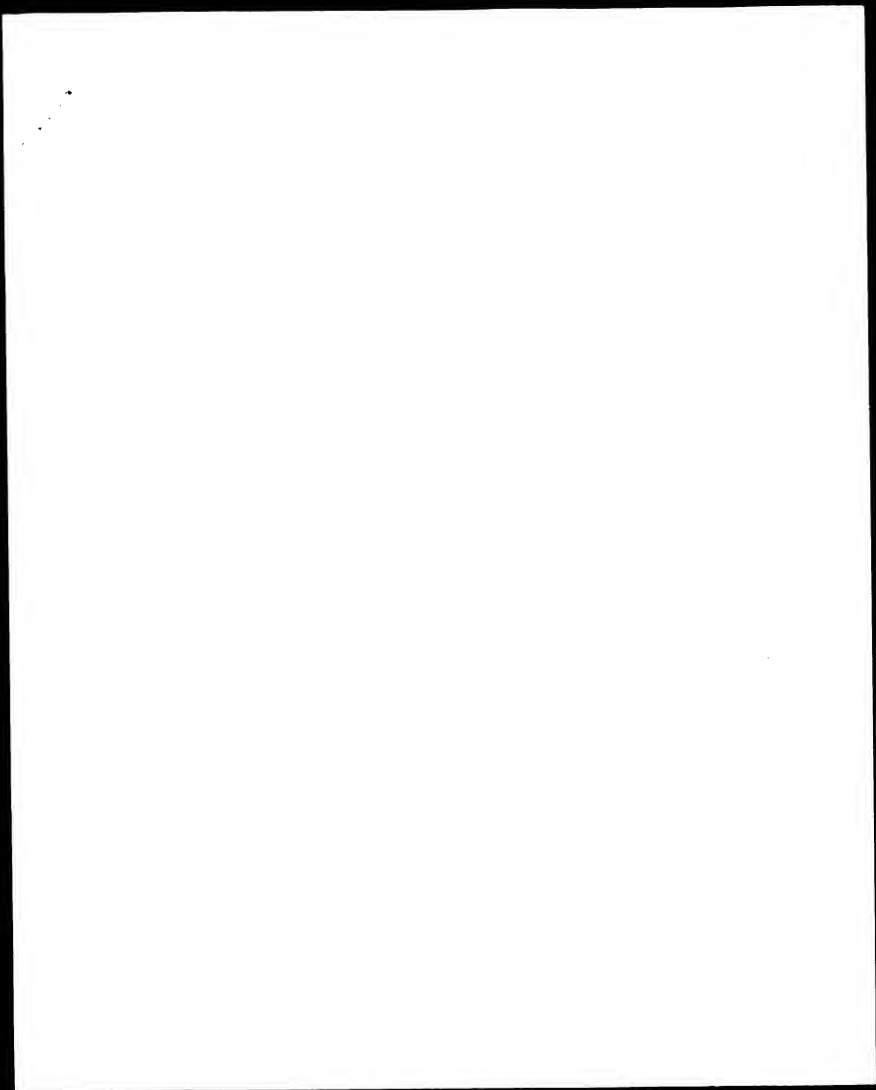
Query Match	Score	DB	Length
19.18;	26;	6;	18;
Best Local Similarity	50.04;		
Best Global Similarity	3.0403;		

Matches	4	Conservative	2	Mismatches	2	Indels	0	Gaps	0
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Oy 9 PKDIVRSI 16

Db 4 PSDVNSTL 11

Search completed: July 15, 2002, 12:53:42
Job time: 198 sec



CC Immediate hypersensitivity, and for immunomodulation.
XX
SQ Sequence 417 Mb.

Query Match 110 Mb, Score 136, DB 18, Length 417,
Best Local Similarity 100.0%, Pred. No. 1a-12 0,
Matches 25: Conservative 0, Mismatches 0, Indels 0, Gaps 0;
OR 1 CCHPHLPHDVSALAKGCRAP 25
|||||
DB 289 CCHPHLPHDVSALAKGCRAP 313

RESULT 4

AA897753 standard; Protein: 426 AA.
XX
XX AA897753;
AC AA897753;
DT 28-MAR-1996 (first entry)
XX
XX Canine IgE.
XX
XX IgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
XX
XX Canis familiaris.
XX
XX W0614867-A1.
XX
XX 21-MAR-1996.
XX
XX PF 03-NOV-1995; 99NO-00313795.
XX
XX PR 09-NOV-1994; 94US-0346891.
XX
XX PR 09-NOV-1994; 94US-0346891.
XX
XX PA (HEAT) MRCCK & CO INC.
XX
XX Hollis GF. Patel MD;
XX
XX WPI: 1996-271371/28.
XX
XX N-PS08; AA72984.
XX
XX New DNA encoding canine IgE and IgA - useful in vaccines, antisense
XX
XX therapy, assays, drug screening, etc.
XX
XX Class 11: Page 29-30; 43pp; English.
XX
XX The canine IgE amino acid sequence (AA897753) was deduced from
XX
XX an isolated gene (AA72984) obtained from a canine liver DNA library.
XX
XX The cloning of the IgE gene allows production of large quantities of
XX
XX recombinant IgE using baculovirus expression systems. This recombinant
XX
XX IgE has been used in the development of drug development (e.g.,
XX
XX small molecule screening, assay development and anti-IgE
XX
XX antibody generation). Fragments of IgE can be used to generate
XX
XX antisera for immunological assays. The amino acid sequence
XX
XX information permits targeted modulation of IgE-mediated immune
XX
XX responses.
XX
XX Sequence 426 Mb;

RESULT 5

Query Match 100.0%, Score 136, DB 17, Length 426,
Best Local Similarity 100.0%, Pred. No. 1a-12;
Matches 25: Conservative 0, Mismatches 0, Indels 0, Gaps 0;
OR 1 CCHPHLPHDVSALAKGCRAP 25
|||||
DB 294 CCHPHLPHDVSALAKGCRAP 316

AA895208
XX
XX AA895208 standard; Protein: 341 AA.
XX
XX AA895208;
AC AA895208;
DT 22-MAY-2000 (first entry)

XX
XX Immunogenic peptide consisting of opsesum CH2, dog CH3 and opsesum CH4.
XX
XX Dog; opsesum; immunoglobulin E; IgE; vaccination; infection; allergy;
XX
XX asthma; eczema; immunogenic peptide.
XX
XX Chimeric - Didiaphis virginiana.
XX
XX Chimeric - Canis sp.
XX
XX W0200023722-A2.
XX
XX PD 11-MAR-2000.
XX
XX PF 21-OCT-1999; 99NO-8201896.
XX
XX PR 03-MAY-1998; 98US-0106452.
XX
XX PR 22-SEP-1999; 99US-0401656.
XX
XX PA (HEAT) MRSISTERTIA PHARM MD.
XX
XX Hellman LT;

XX
XX WPI: 2000-35342/71.
XX
XX

XX
XX Immunogenic polypeptides useful for preventing the harmful effects of
XX
XX immunoglobulin E in mammals -
XX
XX Disclosure: Fig 2; 50pp; English.

XX
XX The present sequence is an immunogenic peptide consisting of the heavy
XX
XX chain constant regions 2 and 4 of the opsesum IgE and the heavy chain
XX
XX constant region 3 from the dog. It was shown to consist of the same
XX
XX regions from one mammal. Immunogenic peptides, particularly those
XX
XX consisting of different heavy chain constant regions, can be used for
XX
XX vaccination, such as asthma, fur, pollen and food allergies and eczema.
XX
XX

XX
XX Sequence 341 Mb;

Query Match 88.6%, Score 120.5, DB 21, Length 341,
Best Local Similarity 88.6%, Pred. No. 1a-12 0,
Matches 24: Conservative 0, Mismatches 1, Indels 1, Gaps 1;
OR 1 CCHPHLPHDVSALAKGCRAP 25
|||||
DB 211 CCHPHLPHDVSALAKGCRAP 316

RESULT 6

AA801643
XX
XX AA801643 standard; Protein: 340 AA.
XX
XX AA801643;
AC AA801643;
DT 22-MAY-2000 (first entry)
XX
XX
XX Rat IgE heavy chain constant regions 2, 3 and 4.
XX
XX Rat; immunoglobulin E; IgE; vaccination; infection; allergy;
XX
XX asthma; eczema; immunogenic peptide.
XX
XX Rat; sp.
XX
XX W0200023722-A2.
XX
XX

RESULT 9
AA060205
ID AA060205 standard: protein: 342 AA.
AC AA060205:
XX 22-NOV-2000 (first entry)
XX 22-NOV-2000 (first entry)
DE Immunogenic peptide consisting of opossum CH2, human CH3 and opossum CH4.
XX human opossum: immunoglobulin E, 19F, vaccination; infection; allergy;
XX asthma; eczema; immunogenic peptide.
XX Chimeric - Didephaps virginiana.
XX Chimeric - Monodelphaps.
XX WC00005722-A2.
PD 11-MAR-2000.
XX 21-OCT-1999. 99MO-SE01866.
XX 02-NOV-1998. 98OS-0106652.
XX 22-SEP-1999. 99OS-0401616.
XX (RESIST-) RESISTENTIA PHARM AB.
XX Helian LT:
XX WPI: 2000-36342/21.
XX Immunogenic polyepitopes useful for preventing the harmful effects of
PT immunoglobulin E in mammals -
XX Disclousure: Fig 2, 50ppr. English.
XX The present sequence is an immunogenic peptide consisting of the heavy
CC chain constant region 2 and 4 of the opossum 19F and the heavy chain
CC constant region 3 from the pig. It was shown to cause a stronger
CC polyclonal anti-salt IgE response than peptides consisting of the same
CC regions from one animal.
XX Immunogenic peptides, particularly those
XX consisting of different heavy chain constant regions, can be used for
CC vaccination in humans, against bacterial and viral infections and
CC allergies, such as asthma, fur, pollen and food allergies and eczema.
XX Sequence 342 AA:
50
Query Match 70.2%; Score 95.5; DB 21; Length 342;
Best Local Similarity 69.2%; Pred. No. 1.5e-06;
Matches 18; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
OY 1 CHTYPIPIADIDYHINAKAKR-AP 25
DB 212 CHTYPIPIADIDYHINAKAKR-AP 25
RESULT 10
AA060207
ID AA060207 standard: protein: 345 AA.
AC AA060207:
XX 22-NOV-2000 (first entry)
XX 22-NOV-2000 (first entry)
DE Immunogenic peptide consisting of opossum CH2, pig CH3 and opossum CH4.
XX pig opossum: immunoglobulin E, 19F; vaccination; infection; allergy;
XX asthma; eczema; immunogenic peptide.
XX Chimeric - Didephaps virginiana.
XX Chimeric - Sus scrofa.

XX WC00005722-A2.
PD 11-MAR-2000.
XX 21-OCT-1999. 99MO-SE01866.
XX 02-NOV-1998. 98OS-0106652.
XX 22-SEP-1999. 99OS-0401616.
XX (RESIST-) RESISTENTIA PHARM AB.
XX Helian LT:
XX WPI: 2000-36342/21.
XX Immunogenic polyepitopes useful for preventing the harmful effects of
PT immunoglobulin E in mammals -
XX Disclousure: Fig 2, 50ppr. English.
XX The present sequence is an immunogenic peptide consisting of the heavy
CC chain constant regions 2 and 4 of the opossum 19F and the heavy chain
CC constant region 3 from the pig. It was shown to cause a stronger
CC polyclonal anti-salt IgE response than peptides consisting of the same
CC regions from one animal.
XX Immunogenic peptides, particularly those
XX consisting of different heavy chain constant regions, can be used for
CC vaccination in humans, against bacterial and viral infections and
CC allergies, such as asthma, fur, pollen and food allergies and eczema.
XX Sequence 345 AA:
50
Query Match 68.8%; Score 93.5; DB 21; Length 345;
Best Local Similarity 72.1%; Pred. No. 3.4e-09;
Matches 19; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
OY 1 CHTYPIPIADIDYHINAKAKR-AP 25
DB 215 CHTYPIPIADIDYHINAKAKR-AP 25
RESULT 11
AA050893
ID AA050893 standard: peptide: 17 AA.
AC AA050893:
XX 24-FEB-2000 (first entry)
XX 24-FEB-2000 (first entry)
DE Antibody 15A.2 binding peptide 10 from phdCite phage display library.
XX Canine: allergy antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
XX epitope; prophylaxis; treatment; minotope.
XX Synthetic.
XX EP957111-A2.
XX 17-NOV-1999.
XX 09-APR-1999. 99BP-0107035.
XX 09-APR-1998. 98BS-0068313.
XX 30-MAR-1999. 99BS-0281760.
XX (IDEX-) IDEX LAB INC.
XX Lawton R. Warner B. Francoeur G.
XX WPI: 2000-04831/04.
XX Binding proteins used for treatment or prophylaxis of canine allergy -

XX Disclosure: Fig 6: 30pp; English.

XX This invention describes a novel binding protein which specifically
 CC binds to canine canine free or B-cell bound IgE, and which does not bind
 CC to dog IgE. The protein is a polypeptide of 156 amino acids. The
 CC invention has anti-allergic activity. The antibodies bind to canine
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reactions. The antibodies bind to canine IgE
 CC and produce a pharmaceutical composition, preferably with an adjuvant, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC Invention: 159900 represent peptide mimotopes used in the method of the
 XX Sequence 17 Ma:

Query Match 65.4% Score 89; DB 21; Length 17;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 1 CYPHOPRODYN1 16
 XX | | | | | | | | | | | | | | | | | |
 DB 2 CYPHOPRODYN1 17

Result 12

XX AM50894 standard; peptide: 17 Ma.

XX AM50894.

XX 24-PRB-2000 (first entry)

XX Antibody 15A.2 canine IgE binding epitope 1.

XX Canine allergy: antibody 15A.2; IgE; B cell; mast cell; anti-allergy;

XX epitope; prophylaxis; treatment; mimotope.

XX Synthetic.

XX EP957111-A2.

XX 09-MAR-1999; 99EP-0107035.

XX 09-MAR-1998; 98US-0058131.

XX 30-MAR-1999; 99US-0281760.

XX (IDEX-) IDEX LAB INC.

XX Landon R. Kerker B. Francoeur G.

XX WPI: 2000-04083704.

XX Binding proteins used for treatment or prophylaxis of canine allergy -

XX Disclosure: Fig 7: 30pp; English.

XX This invention describes a novel binding protein which specifically
 CC binds to active canine free or B-cell bound IgE, and which does not bind
 CC to inactive canine free or B-cell bound IgE. The protein is a polypeptide of 156
 CC amino acids. The invention has anti-allergic activity. The antibodies bind to canine
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reactions. The antibodies bind to canine IgE
 CC and produce a pharmaceutical composition, preferably with an adjuvant, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC Invention: 159900 represent peptide mimotopes used in the method of the
 XX Sequence 17 Ma:

Query Match 65.4% Score 89; DB 21; Length 17;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 1 CYPHOPRODYN1 16
 XX | | | | | | | | | | | | | | | | | |
 DB 2 CYPHOPRODYN1 17

Result 13

XX AM79999 standard; peptide: 23 Ma.

XX AM79999.

XX 15-MAR-2000 (first entry)

XX Optimized 19c-C13 domain antigen peptide for dog IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic antigen;

XX immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

XX anti-allergic; anti-allergy; immunization; anti-allergic;

XX anti-allergic; anti-allergy; asthma; anaphylaxis; dermatitis.

XX Synthetic.

XX MO9967291-AL.

XX 21-JUN-1999; 99MO-0513955.

XX 20-JUN-1998; 98US-0100287.

XX (UNB-) UNITED BIOMEDICAL INC.

XX Wang CY, Wallfield AM;

XX WPI: 2000-160578/14.

XX 19c antigenic peptide from the C13 domain of immunoglobulin E, fusions
 CC for immunization against allergy

XX Claim 1: Page 99; 159pp; English.

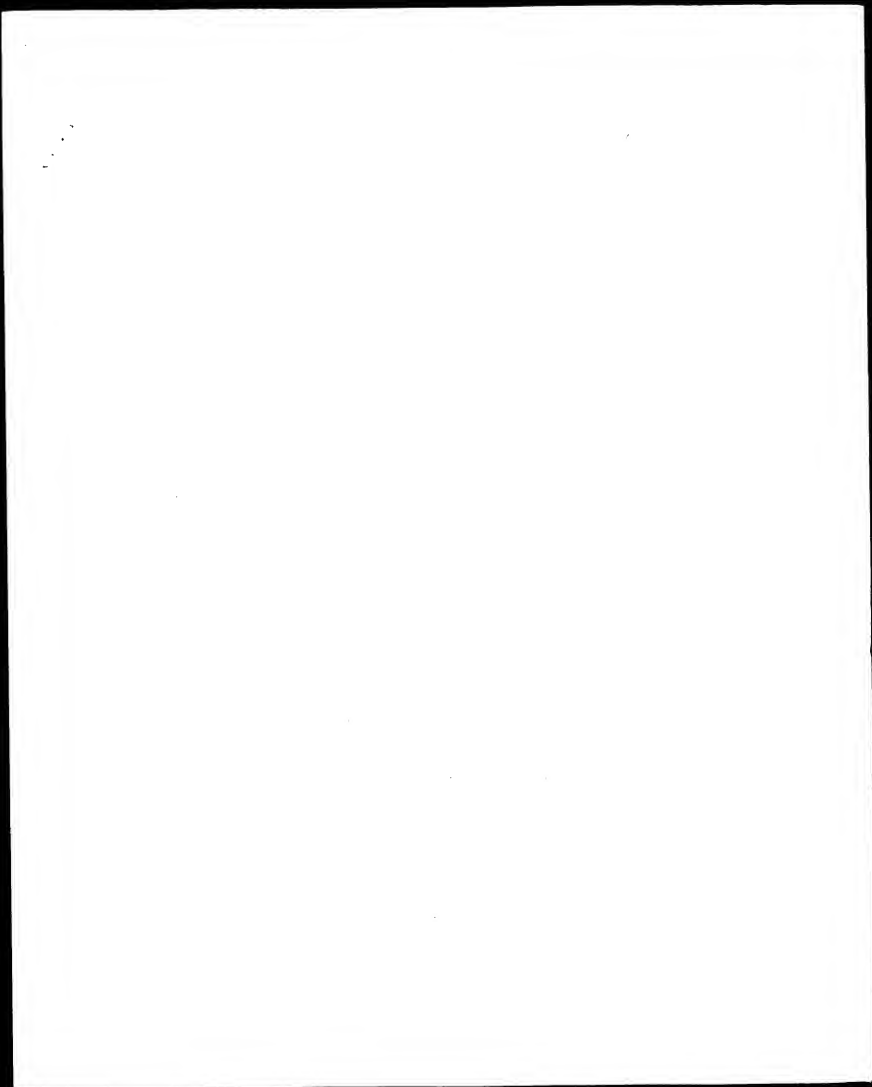
XX The present invention describes immunoglobulin E (IgE)-C13 domain
 CC antigenic peptide (1). (1) have anti-allergic, anti-anaphylactic
 CC activity, and are useful for the treatment of allergic diseases, IgE,
 CC specific for a target effector site on canine polyclonal antibodies
 CC and so preventing triggering and activation of mast cells and eosinophils
 CC and downregulation of IgE synthesis. Conjugates or fusion peptides,
 CC conjugates or fusion peptides, conjugates or fusion peptides, conjugates
 CC or fusion peptides, conjugates or fusion peptides, conjugates or fusion
 CC peptides, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC conjugates of (1) that include a proinflammatory T helper cell epitope.
 CC (functional in genetically diverse subjects). In addition to a B cell
 CC conjugate of (1) that include a proinflammatory T helper cell epitope,
 CC conjugates of (1) that include a proinflammatory T helper cell epitope
 CC (non-anaphylactic) antibodies. AM79999 to AM9084 represent amino
 CC acid sequences used in the amplification of the present invention.

XX Sequence 23 Ma:

Query Match 65.4% Score 89; DB 21; Length 25;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 2 RYRHPKQVSYINX 18




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RESULT 2
SEQUENCE 2: Application: PC/MS951795
GENERAL INFORMATION: GREGORY F.
APPLICANT: PATIL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
CORRESPONDENCE ADDRESS:
ADDRESS: CHRISTINE E. CARY
STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
STATE: NEW JERSEY
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release 11.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
NAME: CARY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
TELEPHONE: (608) 594-6734
TELEFAX: (608) 594-6720
INVENTOR: CARY, CHRISTINE E.
SEQUENCE CHARACTERISTICS: 2:
LENGTH: 426 amino acids
STRANDS: single
TOPOLOGY: linear
REMARKS: Type: Protein
PC-MS951795-2

Query Match
Best Local Similarity: 100.0% Score 136; DB 5; Length 476;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CENTHRLPPIALNSALAKSNAP 25
DB 294 CENTHRLPPIALNSALAKSNAP 318

RESULT 3
SEQUENCE 3: Application: US/0823239D
Patent No. 5955709
GENERAL INFORMATION:
APPLICANT: Freese, Leonard G.
APPLICANT: Jarcou, Paula M.
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
CITY: South San Francisco
STATE: California
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Genentech
Current Application Data:

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APPLICATION NUMBER: US/08/232,390D
CLASSIFICATION: 530
PRIOR APPLICATION DATA: 07/58/1953
APPLICATION NUMBER: 07/58-1954
PRIOR APPLICATION DATA: 07/44/768
ATTORNEY/AGENT INFORMATION:
NAME: Syngenta, C219 G.
REFERENCE/DOCKET NUMBER: P07183
TELECOMMUNICATION INFORMATION:
TELEPHONE: 602/957-9681
SEQUENCE CHARACTERISTICS:
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-232-390-04

Query Match
Best Local Similarity: 61.94; Score 78; DB 3; Length 106;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
1 CENTHRLPPIALNSALAKSNAP 21
DB 84 CENTHRLPPIALNSALAKSNAP 104

RESULT 4
US-08-466-163-3
SEQUENCE 4: Application: US/08466163B
Patent No. 6239309
GENERAL INFORMATION:
APPLICANT: Freese, Leonard G.
APPLICANT: Jarcou, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
CURRENT FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-10-15
PRIOR APPLICATION NUMBER: US/08/185,899
PRIOR FILING DATE: 1992-05-07
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US/07/44,768
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 1
TYPE: Protein
ORGANISM: Homo sapiens
US-08-466-163-1

Query Match
Best Local Similarity: 57.44; Score 78; DB 4; Length 109;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
1 CENTHRLPPIALNSALAKSNAP 21
DB 88 CENTHRLPPIALNSALAKSNAP 108

RESULT 5
US-08-232-390-05
SEQUENCE 5: Application: US/0823239D
Patent No. 5955709

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1      FILING DATE: 30-APR-1999
2      CLASSIFICATION DATA:
3      APPLICATION NUMBER: 09/100,414
4      FILING DATE: 20-JUNE-1998
5      INVENTOR: MORGAN, L.L.P.
6      NAME: Mella H. Llin
7      REGISTRATION NUMBER: 29,323
8      TELEPHONE: 212-758-4800
9      TELECOMMUNICATION INFORMATION:
10     INFORMATION SOURCE: 98:
11     SEQUENCE CHARACTERISTICS:
12     LENGTH: 42 amino acids
13     TOPOLOGY: linear
14     MOLECULE TYPE: peptide
15     US-09-303-323-98

Query Match 47 1%; Score 64; DB 4; Length 42;
Query Similarity 64.7%; Pval 0.0023;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 25 NITRILIPALAMSTRK 41

RESULT 14
US-09-303-323-99
US-09-303-323-99 Application US/0930323
Patent No. 628887
GENERAL INFORMATION: China X1
TITLE OF INVENTION: NOVEL LIPID PEPTIDE
INVENTOR: MORGAN, L.L.P.
CORRESPONDENCE ADDRESS: 106
ADDRESSER: Morgan & Flanagan, L.L.P.
STREET: 345 Park Avenue
STATE: NY 10017
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
FILING DATE: 30-APR-1999
CLASSIFICATION DATA:
REGISTRATION/DOCKET NUMBER: 29,323
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
INVENTOR: MORGAN, L.L.P.
NAME: Mella H. Llin
REGISTRATION/DOCKET NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELECOMMUNICATION INFORMATION:
INFORMATION SOURCE: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-99

Query Match 47 1%; Score 64; DB 4; Length 42;
Query Similarity 64.7%; Pval 0.0023;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 25 NITRILIPALAMSTRK 41

RESULT 15
US-09-303-323-100
US-09-303-323-100 Application US/0930323
Patent No. 628887
GENERAL INFORMATION: China X1
TITLE OF INVENTION: NOVEL LIPID PEPTIDE
INVENTOR: MORGAN, L.L.P.
CORRESPONDENCE ADDRESS: 106
ADDRESSER: Morgan & Flanagan, L.L.P.
STREET: 345 Park Avenue
STATE: NY 10017
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
FILING DATE: 30-APR-1999
CLASSIFICATION DATA:
REGISTRATION/DOCKET NUMBER: 29,323
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
INVENTOR: MORGAN, L.L.P.
NAME: Mella H. Llin
REGISTRATION/DOCKET NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELECOMMUNICATION INFORMATION:
INFORMATION SOURCE: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-100

Query Match 47 1%; Score 64; DB 4; Length 42;
Query Similarity 64.7%; Pval 0.0023;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 25 NITRILIPALAMSTRK 41

Search completed: July 15, 2002, 12:45:40
000 time: 21 sec

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Mon Jul 15 13:22:27 2002

us-09-938-700-4.open.ral

Page 4

SEQUENCE CHARACTERISTICS:
NUMBER OF RESIDUES: 408
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-444-02A-1

Query Match 1: 48 64; Score 67.5; DB 2; Length 119;

US-09-100-414B-95 Similarity 50.74; Pct Ident 0.0022; Mismatches 5; Indels 1; Gaps 1;

Matches 13; Conservative 21

DB 97 CAYTBLP.PALMKNSTKTS 118

RESULT 8

US-09-100-414B-95
US-09-100-414B-95 Application US/09100414B
Patent No. 6025466

GENERAL INFORMATION: CHUNG YI

TITLE OF INVENTION: NOVEL LHRH PEPTIDE

TELECOMMUNICATION INFORMATION: 106

ADDRESSER: Morgan & Flinnegan, L.L.P.

STREET: 345 Park Avenue

STATE: NY

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC Windows

SOFTWARE: Word 97

CURRENT APPLICATION DATA:

FILING DATE: 20-JUNE-1998

CLASSIFICATION: 424

NAME: Maria H. Lin

REGISTRATION NUMBER: 29,323

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800

INFORMATION: 95

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TOPOLOGY: Linear

MOLECULE TYPE: Peptide

US-09-100-414B-95

Query Match 1: 47 13; Score 64; DB 3; Length 25;

US-09-100-414B-95 Similarity 47.14; Pct Ident 0.0012; Mismatches 11; Conservative 3; Indels 0; Gaps 0;

Matches 11; Conservative 3; Indels 0; Gaps 0;

DB 8 RYTHMHPALMKNSTK 24

TITLE OF INVENTION: IMMUNOGENS
NUMBER OF RESIDUES: 408
CORRESPONDENCE ADDRESS: 106
ADDRESSER: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
STATE: NY
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
NAME: Maria H. Lin

US-09-100-414B-95
US-09-100-414B-95 Application US/09100414B
Patent No. 6025466
GENERAL INFORMATION: CHUNG YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TELECOMMUNICATION INFORMATION: 106
ADDRESSER: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
STATE: NY
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
NAME: Maria H. Lin

Query Match 1: 47 13; Score 64; DB 4; Length 25;

US-09-100-414B-95 Similarity 47.14; Pct Ident 0.0012; Mismatches 11; Conservative 3; Indels 0; Gaps 0;

Matches 11; Conservative 3; Indels 0; Gaps 0;

DB 8 RYTHMHPALMKNSTK 24

Genome version 4.5
Copyright (c) 1999 - 2000 Comagen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 12:45:19 ; Search time 15.25 seconds
(without alignments)

157,573 Million cell updates/sec

Title: US-09-938-700-4

Perfect score: 136

Sequence: 1 CERVHILKQIVSYAKNGKRP 25

Scoring table: BLOSUM62

Gap: 10.0, Gapex: 0.5

Search: 28318 seqs, 9608934 residues

28318

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Deleting first 5 summaries

Database: PIR, J1, *

1: p1r1*

2: p1r1*

3: p1r1*

4: p1r1*

Pred. No. is the number of results predicted by chance 10 have 3
score greater than or equal to the predicted score.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	77.2	429	1 EHRT	19 epsilon chain C
2	89	65.4	428	2 13R48	19 epsilon chain C
3	86	59.8	388	1 EHMS	19 epsilon chain C
4	80	58.8	548	2 53R64	19 epsilon chain C
5	67	49.3	107	2 16R726	19 epsilon chain C
6	59	43.4	684	2 86Q266	19 epsilon chain C
7	58	42.6	138	1 50R005	19 epsilon chain C
8	54	39.7	1399	1 A46762	19 epsilon chain C
9	54	39.7	1399	1 A46762	19 epsilon chain C
10	54	39.7	1399	1 A46762	19 epsilon chain C
11	54	39.7	1399	1 A46762	19 epsilon chain C
12	54	39.7	1399	1 A46762	19 epsilon chain C
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14	54	39.7	1399	1 A46762	19 epsilon chain C
15	51	37.5	579	2 B46529	19 epsilon chain C
16	51	37.5	579	2 B46529	19 epsilon chain C
17	51	37.5	579	2 B46529	19 epsilon chain C
18	51	37.5	579	2 B46529	19 epsilon chain C
19	50.5	37.1	327	1 64R42	19 gamma-4 chain C
20	50.5	37.1	327	1 64R42	19 gamma-4 chain C
21	50.5	37.1	328	2 147161	19 gamma-1 chain C
22	50.5	37.1	328	2 147161	19 gamma-1 chain C
23	50.5	37.1	328	2 147161	19 gamma-1 chain C
24	50.5	37.1	328	2 147161	19 gamma-1 chain C
25	50.5	37.1	330	1 G2MSM	19 gamma-2 chain C
26	50.5	37.1	446	2 58Q355	19 gamma-2 chain C
27	50.5	37.1	446	2 58Q355	19 gamma-2 chain C
28	50.5	37.1	446	2 58Q355	19 gamma-2 chain C
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36	49.5	36.4	405	1 G2MSM	19 gamma-2b chain
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83	48.5	35.7	1938	1 20J178	myosin heavy chain
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98	48.5	35.7	1938	1 20J178	myosin heavy chain
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ALIGNMENTS

RESULT 1

EHRT

C:Species: 19 epsilon chain C region - rat

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using SW model

Run on: July 15, 2002, 12:46:19 ; Search time 10.41 Seconds
(without alignment)

92.986 Million cell updates/sec

Title: DS-09-938-700-4
Perfect score: 136

Sequence: 1 CRVTHPLPKDIVRSIAKAPGKRAP 2:

Scoring table:

	BLOSUM62	Gamert
Cano 10	0	0

Scanned with CamScanner

total number of hits at each chosen parameters

Minimum PR seg length = 0

Maximum DB seq length: 2000000000

Post-processing:	Minimum Match	Maximum Match
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1	0	10
2	0	10
3	0	10
4	0	10
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92	0	10
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95	0	10
96	0	10
97	0	10
98	0	10
99	0	10

Listing 4.1: First 45

Database : SWISSPROT_40:

Prod. No. is the number of
score greater than or equal

and is derived by analysis of the total score distribution.

SUMMARIES

Query	Answer
1. What is the main purpose of the study?	The main purpose of the study is to investigate the effect of the proposed method on the performance of the system.
2. What are the research objectives?	The research objectives are to compare the proposed method with the existing methods and to evaluate the performance of the system.
3. What is the scope of the study?	The scope of the study is limited to the performance of the system under different conditions.
4. What are the limitations of the study?	The limitations of the study are that the results are only valid for the specific conditions and that the study is only a preliminary investigation.
5. What are the conclusions of the study?	The conclusions of the study are that the proposed method is effective and that the system performs well under different conditions.

SUMMARY

Rank	Score	Length	ID	Description
1	105	772	LOC_101951	LOC_101951
2	80	568	LOC_101952	LOC_101952
3	80	568	LOC_101953	LOC_101953
4	54	391	LOC_101954	LOC_101954
5	54	391	LOC_101955	LOC_101955
6	34	397	LOC_101956	LOC_101956
7	34	397	LOC_101957	LOC_101957
8	51	375	LOC_101958	LOC_101958
9	51	375	LOC_101959	LOC_101959
10	50	368	LOC_101960	LOC_101960
11	50	368	LOC_101961	LOC_101961
12	50	368	LOC_101962	LOC_101962
13	50	368	LOC_101963	LOC_101963
14	50	368	LOC_101964	LOC_101964
15	50	368	LOC_101965	LOC_101965
16	50	368	LOC_101966	LOC_101966
17	49	364	LOC_101967	LOC_101967
18	49	364	LOC_101968	LOC_101968
19	49	364	LOC_101969	LOC_101969
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FT 41960 42009
FT 42010 42059
FT 42060 42109
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FT 42160 42209
FT 42210 42259
FT 42260 42309
FT 4

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OW protein - protein search, using sw method

Run on: July 15, 2002, 12:45:44 ; Search time 25.08 seconds

(without alignment)
12.443 Million CDS updates/sec

Title: US-09-938-700-4

Perfect score: 116 GYVYHPRHEDVWISAKNCRGP 25

Sequence: 16 GYVYHPRHEDVWISAKNCRGP 25

Scoring table: BLOSUM62

Gap: 10.0, Gapex: 0.5

Total number of hits satisfying chosen parameters: 56222

Millam DB seq length: 0

Millam DB seq length: 20000000

Post-processing: Millam NCH 08

Listing first 45 summaries

Database: 1: SP archaea;
2: SP bacteria;
3: SP fungi;
4: SP protozoa;
5: SP invertebrates;
6: SP mammals;
7: SP plants;
8: SP algae;
9: SP phage;
10: SP virus;
11: SP eukaryotes;
12: SP eukaryotes;
13: SP eukaryotes;
14: SP eukaryotes;
15: SP eukaryotes;
16: SP eukaryotes;
17: SP eukaryotes;
18: SP eukaryotes;
19: SP eukaryotes;
20: SP eukaryotes;
21: SP eukaryotes;
22: SP eukaryotes;
23: SP eukaryotes;
24: SP eukaryotes;
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33: SP eukaryotes;
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35: SP eukaryotes;
36: SP eukaryotes;
37: SP eukaryotes;
38: SP eukaryotes;
39: SP eukaryotes;
40: SP eukaryotes;
41: SP eukaryotes;
42: SP eukaryotes;
43: SP eukaryotes;
44: SP eukaryotes;
45: SP eukaryotes;

SUMMARIES

Result	No.	Score	Match	Length	ID	Description
1	59	43.4	684	13	090544	090544 ginseng
2	54	39.7	59	6	090544	090544 ginseng
3	54	39.7	59	6	090544	090544 ginseng
4	51	37.5	187	2	092838	092838 streptococcus
5	50	37.1	538	16	092838	092838 streptococcus
6	50	36.8	1038	6	092839	092839 streptococcus
7	50	36.8	1038	6	092839	092839 streptococcus
8	50	36.8	1038	6	092839	092839 streptococcus
9	50	36.8	1038	6	092839	092839 streptococcus
10	50	36.8	1038	6	092839	092839 streptococcus
11	49	36.8	1038	6	092839	092839 streptococcus
12	49	36.8	1038	6	092839	092839 streptococcus
13	49	36.8	1038	6	092839	092839 streptococcus
14	49	36.8	1038	6	092839	092839 streptococcus
15	49	36.8	1038	6	092839	092839 streptococcus
16	49	36.8	1038	6	092839	092839 streptococcus

ALIGNMENTS

Result	ID	Score	Match	Length	ID	Description
1	090544	43.4	684	13	090544	090544 ginseng
2	090544	39.7	59	6	090544	090544 ginseng
3	090544	39.7	59	6	090544	090544 ginseng
4	090544	37.5	187	2	092838	092838 streptococcus
5	090544	37.1	538	16	092838	092838 streptococcus
6	090544	36.8	1038	6	092839	092839 streptococcus
7	090544	36.8	1038	6	092839	092839 streptococcus
8	090544	36.8	1038	6	092839	092839 streptococcus
9	090544	36.8	1038	6	092839	092839 streptococcus
10	090544	36.8	1038	6	092839	092839 streptococcus
11	090544	36.8	1038	6	092839	092839 streptococcus
12	090544	36.8	1038	6	092839	092839 streptococcus
13	090544	36.8	1038	6	092839	092839 streptococcus
14	090544	36.8	1038	6	092839	092839 streptococcus
15	090544	36.8	1038	6	092839	092839 streptococcus
16	090544	36.8	1038	6	092839	092839 streptococcus

Match 11: Conservative 4: Mismatches 7: Indels 0: Gaps 0:
 QY 1 CATTGHHKQVWYINAKRCK 22
 |||||:||||:|
 DB 645 CATTGHHKQVWYINAKRCK 666

RESULT 2

ID 09H55 PRELIMINARY: PRT: 99 NA.

OC 09H55-2000 (TREMURel. 15, Created)
 DT 01-OCT-2000 (TREMURel. 15, Last sequence update)
 DT 01-DEC-2000 (TREMURel. 19, Last annotation update)
 GN MYRIN HEAVY CHAIN (PDBCODE: 1).

OS Oryctolagus cuniculus (rabbit).
 OC Myriophoridae: Chorodae: Vertebrata: Euteleostomi:
 OC Mammalia: Lagomorpha: Leporidae: Oryctolagus.
 OX Ncbi_TextID=9566.

SEQUENCE FROM N.A.

NA STRAIN=NMN ZEALAND WHITE: TISSUE=HEART;
 NA Sayed R.A., Grace A.A., Vandenberg J.T.;
 NA 1996, J. Mol. Biol. 260:1-12, Expression in cardiac hypertrophy.
 RU Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ293117, CNA94849.1.
 DR InterPro: IPR000109: myosin head.
 DR Pfam: PF00053: myosin head 1.
 DR ProDom: PD00035: myosin head 1.
 FT NON_TER 99
 FT NON_TER 99
 SO SEQUENCE 99 NA, 10933 MW: 3961CA1047D2BDC CCK64:

Query Match
 Best Local Similarity 39.7% Score 54: DB 6: Length 99:
 Matches 10 Conservative 3: Mismatches 7: Indels 0: Gaps 0:

QY 2 VYTHPRHGLQVYINAKRCK 21
 |||||:||||:|
 DB 73 VYTHPRHGLQVYINAKRCK 98

RESULT 3

ID 09AH3 PRELIMINARY: PRT: 273 NA.

OC 09AH3-2000 (TREMURel. 17, Created)
 DT 01-JUN-2001 (TREMURel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMURel. 17, Last annotation update)
 DB HYPOPHYSAL PROTEIN CCK64.

SEQUENCE FROM N.A.

NA STRAIN=NMN ZEALAND WHITE: TISSUE=HEART;
 NA Nierman M.C., Feldblum T.V., Land M.T., Paulsen I.T., Nelson K.E.,
 NA 1996, J. Biol. Chem. 271:15967-15971, Expression in cardiac hypertrophy.
 RU Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ293117, CNA94849.1.
 DR InterPro: IPR000109: myosin head.
 DR Pfam: PF00053: myosin head 1.
 DR ProDom: PD00035: myosin head 1.
 FT NON_TER 99
 FT NON_TER 99
 SO SEQUENCE 99 NA, 10933 MW: 3961CA1047D2BDC CCK64:

Query Match
 Best Local Similarity 38.2% Score 52: DB 16: Length 173:
 Matches 10: Conservative 5: Mismatches 4: Indels 10: Gaps 2:

QY 4 THPRHGLQVYINAKRCK 25
 |||||:||||:|
 DB 224 THPRHGLQVYINAKRCK 255

RESULT 4

ID 092B8 PRELIMINARY: PRT: 197 NA.

OC 092B8-2000 (TREMURel. 10, Created)
 DT 01-MAY-1999 (TREMURel. 10, Last sequence update)
 DT 01-DEC-2000 (TREMURel. 15, Last annotation update)
 GN MYRIN HEAVY CHAIN (PDBCODE: 1).

OS Oryctolagus cuniculus (rabbit).
 OC Myriophoridae: Chorodae: Vertebrata: Euteleostomi:
 OC Mammalia: Lagomorpha: Leporidae: Oryctolagus.
 OX Ncbi_TextID=9566.

SEQUENCE FROM N.A.

NA STRAIN=NMN ZEALAND WHITE: TISSUE=HEART;
 NA Bentley S.D., Parkhill J., Barrett B.G., Rojandream M.A.,
 NA 1999, Nature 398:332-339, Expression in cardiac hypertrophy.
 RU Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ293117, CNA94849.1.
 DR InterPro: IPR000109: myosin head.
 DR Pfam: PF00053: myosin head 1.
 DR ProDom: PD00035: myosin head 1.
 FT NON_TER 99
 FT NON_TER 99
 SO SEQUENCE 99 NA, 10933 MW: 3961CA1047D2BDC CCK64:

Query Match
 Best Local Similarity 42.9% Score 51: DB 2: Length 173:
 Matches 5: Conservative 6: Mismatches 6: Indels 0: Gaps 0:

QY 3 VYTHPRHGLQVYINAKRCK 23
 |||||:||||:|
 DB 177 VYTHPRHGLQVYINAKRCK 197

RESULT 5

ID 09H55 PRELIMINARY: PRT: 538 NA.

OC 09H55-2000 (TREMURel. 15, Created)
 DT 01-OCT-2000 (TREMURel. 15, Last sequence update)
 DT 01-DEC-2000 (TREMURel. 15, Last annotation update)
 GN MYRIN HEAVY CHAIN (PDBCODE: 1).

OS Oryctolagus cuniculus (rabbit).
 OC Myriophoridae: Chorodae: Vertebrata: Euteleostomi:
 OC Mammalia: Lagomorpha: Leporidae: Oryctolagus.
 OX Ncbi_TextID=9566.

NA STRAIN=NMN ZEALAND WHITE: TISSUE=HEART;
 NA Bentley S.D., Parkhill J., Barrett B.G., Rojandream M.A.,
 NA 1999, Nature 398:332-339, Expression in cardiac hypertrophy.
 RU Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ293117, CNA94849.1.
 DR InterPro: IPR000109: myosin head.
 DR Pfam: PF00053: myosin head 1.
 DR ProDom: PD00035: myosin head 1.
 FT NON_TER 99
 FT NON_TER 99
 SO SEQUENCE 99 NA, 10933 MW: 3961CA1047D2BDC CCK64:

Query Match
 Best Local Similarity 40.6% Score 50: DB 16: Length 173:
 Matches 10: Conservative 5: Mismatches 4: Indels 10: Gaps 2:

QY 4 THPRHGLQVYINAKRCK 25
 |||||:||||:|
 DB 224 THPRHGLQVYINAKRCK 255

RESULT 6

ID 092B8 PRELIMINARY: PRT: 197 NA.

OC 092B8-2000 (TREMURel. 10, Created)
 DT 01-MAY-1999 (TREMURel. 10, Last sequence update)
 DT 01-DEC-2000 (TREMURel. 15, Last annotation update)
 GN MYRIN HEAVY CHAIN (PDBCODE: 1).

OS Oryctolagus cuniculus (rabbit).
 OC Myriophoridae: Chorodae: Vertebrata: Euteleostomi:
 OC Mammalia: Lagomorpha: Leporidae: Oryctolagus.
 OX Ncbi_TextID=9566.

NA STRAIN=NMN ZEALAND WHITE: TISSUE=HEART;
 NA Bentley S.D., Parkhill J., Barrett B.G., Rojandream M.A.,
 NA 1999, Nature 398:332-339, Expression in cardiac hypertrophy.
 RU Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ293117, CNA94849.1.
 DR InterPro: IPR000109: myosin head.
 DR Pfam: PF00053: myosin head 1.
 DR ProDom: PD00035: myosin head 1.
 FT NON_TER 99
 FT NON_TER 99
 SO SEQUENCE 99 NA, 10933 MW: 3961CA1047D2BDC CCK64:

Query Match
 Best Local Similarity 40.6% Score 50: DB 16: Length 173:
 Matches 10: Conservative 5: Mismatches 4: Indels 10: Gaps 2:

QY 4 THPRHGLQVYINAKRCK 25
 |||||:||||:|
 DB 224 THPRHGLQVYINAKRCK 255

OC 092B8-2000 (TREMURel. 10, Created)
 DT 01-MAY-1999 (TREMURel. 10, Last sequence update)
 DT 01-DEC-2000 (TREMURel. 15, Last annotation update)
 GN MYRIN HEAVY CHAIN (PDBCODE: 1).

OS Oryctolagus cuniculus (rabbit).
 OC Myriophoridae: Chorodae: Vertebrata: Euteleostomi:
 OC Mammalia: Lagomorpha: Leporidae: Oryctolagus.
 OX Ncbi_TextID=9566.

NA STRAIN=NMN ZEALAND WHITE: TISSUE=HEART;
 NA Bentley S.D., Parkhill J., Barrett B.G., Rojandream M.A.,
 NA 1999, Nature 398:332-339, Expression in cardiac hypertrophy.
 RU Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ293117, CNA94849.1.
 DR InterPro: IPR000109: myosin head.
 DR Pfam: PF00053: myosin head 1.
 DR ProDom: PD00035: myosin head 1.
 FT NON_TER 99
 FT NON_TER 99
 SO SEQUENCE 99 NA, 10933 MW: 3961CA1047D2BDC CCK64:

Query Match
 Best Local Similarity 40.6% Score 50: DB 16: Length 173:
 Matches 10: Conservative 5: Mismatches 4: Indels 10: Gaps 2:

QY 4 THPRHGLQVYINAKRCK 25
 |||||:||||:|
 DB 224 THPRHGLQVYINAKRCK 255

OC 092B8-2000 (TREMURel. 10, Created)
 DT 01-MAY-1999 (TREMURel. 10, Last sequence update)
 DT 01-DEC-2000 (TREMURel. 15, Last annotation update)
 GN MYRIN HEAVY CHAIN (PDBCODE: 1).

OS Oryctolagus cuniculus (rabbit).
 OC Myriophoridae: Chorodae: Vertebrata: Euteleostomi:
 OC Mammalia: Lagomorpha: Leporidae: Oryctolagus.
 OX Ncbi_TextID=9566.

NA STRAIN=NMN ZEALAND WHITE: TISSUE=HEART;
 NA Bentley S.D., Parkhill J., Barrett B.G., Rojandream M.A.,
 NA 1999, Nature 398:332-339, Expression in cardiac hypertrophy.
 RU Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ293117, CNA94849.1.
 DR InterPro: IPR000109: myosin head.
 DR Pfam: PF00053: myosin head 1.
 DR ProDom: PD00035: myosin head 1.
 FT NON_TER 99
 FT NON_TER 99
 SO SEQUENCE 99 NA, 10933 MW: 3961CA1047D2BDC CCK64:

Query Match
 Best Local Similarity 40.6% Score 50: DB 16: Length 173:
 Matches 10: Conservative 5: Mismatches 4: Indels 10: Gaps 2:

QY 4 THPRHGLQVYINAKRCK 25
 |||||:||||:|
 DB 224 THPRHGLQVYINAKRCK 255

[illegible]